

Yonatan H Grad

List of Publications by Year in descending order

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Version: 2024-02-01

124
papers

9,941
citations

66343

42
h-index

48315

88
g-index

188
all docs

188
docs citations

188
times ranked

15785
citing authors

#	ARTICLE	IF	CITATIONS
1	Projecting the transmission dynamics of SARS-CoV-2 through the postpandemic period. <i>Science</i> , 2020, 368, 860-868.	12.6	2,103
2	Model-informed COVID-19 vaccine prioritization strategies by age and serostatus. <i>Science</i> , 2021, 371, 916-921.	12.6	588
3	Identification of many microRNAs that copurify with polyribosomes in mammalian neurons. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 360-365.	7.1	528
4	Aggregated mobility data could help fight COVID-19. <i>Science</i> , 2020, 368, 145-146.	12.6	303
5	Computational and Experimental Identification of <i>C. elegans</i> microRNAs. <i>Molecular Cell</i> , 2003, 11, 1253-1263.	9.7	289
6	Genomic epidemiology of the <i>Escherichia coli</i> O104:H4 outbreaks in Europe, 2011. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 3065-3070.	7.1	262
7	The novel 2016 WHO <i>Neisseria gonorrhoeae</i> reference strains for global quality assurance of laboratory investigations: phenotypic, genetic and reference genome characterization. <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 3096-3108.	3.0	246
8	Cross-reactive memory T cells and herd immunity to SARS-CoV-2. <i>Nature Reviews Immunology</i> , 2020, 20, 709-713.	22.7	229
9	Comparing nonpharmaceutical interventions for containing emerging epidemics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 4023-4028.	7.1	219
10	Viral Dynamics of SARS-CoV-2 Variants in Vaccinated and Unvaccinated Persons. <i>New England Journal of Medicine</i> , 2021, 385, 2489-2491.	27.0	216
11	Genomic epidemiology of <i>Neisseria gonorrhoeae</i> with reduced susceptibility to cefixime in the USA: a retrospective observational study. <i>Lancet Infectious Diseases</i> , The, 2014, 14, 220-226.	9.1	193
12	Genomic Epidemiology of Gonococcal Resistance to Extended-Spectrum Cephalosporins, Macrolides, and Fluoroquinolones in the United States, 2000–2013. <i>Journal of Infectious Diseases</i> , 2016, 214, 1579-1587.	4.0	186
13	Origin and Proliferation of Multiple-Drug Resistance in Bacterial Pathogens. <i>Microbiology and Molecular Biology Reviews</i> , 2015, 79, 101-116.	6.6	183
14	WGS to predict antibiotic MICs for <i>Neisseria gonorrhoeae</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 1937-1947.	3.0	169
15	Individual quarantine versus active monitoring of contacts for the mitigation of COVID-19: a modelling study. <i>Lancet Infectious Diseases</i> , The, 2020, 20, 1025-1033.	9.1	168
16	Multi-institute analysis of carbapenem resistance reveals remarkable diversity, unexplained mechanisms, and limited clonal outbreaks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 1135-1140.	7.1	158
17	Whole-genome sequencing to determine transmission of <i>Neisseria gonorrhoeae</i> : an observational study. <i>Lancet Infectious Diseases</i> , The, 2016, 16, 1295-1303.	9.1	149
18	Estimating the proportion of bystander selection for antibiotic resistance among potentially pathogenic bacterial flora. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11988-E11995.	7.1	141

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19	Azithromycin Resistance through Interspecific Acquisition of an Epistasis-Dependent Efflux Pump Component and Transcriptional Regulator in <i>Neisseria gonorrhoeae</i> . <i>MBio</i> , 2018, 9, .	4.1	133
20	Viral dynamics of acute SARS-CoV-2 infection and applications to diagnostic and public health strategies. <i>PLoS Biology</i> , 2021, 19, e3001333.	5.6	133
21	Clinically prevalent mutations in <i>Mycobacterium tuberculosis</i> alter propionate metabolism and mediate multidrug tolerance. <i>Nature Microbiology</i> , 2018, 3, 1032-1042.	13.3	132
22	The distribution of antibiotic use and its association with antibiotic resistance. <i>ELife</i> , 2018, 7, .	6.0	132
23	Secular Trends in <i>Helicobacter pylori</i> Seroprevalence in Adults in the United States: Evidence for Sustained Race/Ethnic Disparities. <i>American Journal of Epidemiology</i> , 2012, 175, 54-59.	3.4	128
24	Reductions in commuting mobility correlate with geographic differences in SARS-CoV-2 prevalence in New York City. <i>Nature Communications</i> , 2020, 11, 4674.	12.8	105
25	Vaccine waning and mumps re-emergence in the United States. <i>Science Translational Medicine</i> , 2018, 10, .	12.4	101
26	Concerns about SARS-CoV-2 evolution should not hold back efforts to expand vaccination. <i>Nature Reviews Immunology</i> , 2021, 21, 330-335.	22.7	98
27	The impact of antimicrobials on gonococcal evolution. <i>Nature Microbiology</i> , 2019, 4, 1941-1950.	13.3	91
28	Rapid inference of antibiotic resistance and susceptibility by genomic neighbour typing. <i>Nature Microbiology</i> , 2020, 5, 455-464.	13.3	74
29	Bridging of <i>Neisseria gonorrhoeae</i> lineages across sexual networks in the HIV pre-exposure prophylaxis era. <i>Nature Communications</i> , 2019, 10, 3988.	12.8	69
30	Comparative Genomics of Recent Shiga Toxin-Producing <i>Escherichia coli</i> O104:H4: Short-Term Evolution of an Emerging Pathogen. <i>MBio</i> , 2013, 4, e00452-12.	4.1	68
31	Multi-strain Tn-Seq reveals common daptomycin resistance determinants in <i>Staphylococcus aureus</i> . <i>PLoS Pathogens</i> , 2019, 15, e1007862.	4.7	68
32	Evaluation of parameters affecting performance and reliability of machine learning-based antibiotic susceptibility testing from whole genome sequencing data. <i>PLoS Computational Biology</i> , 2019, 15, e1007349.	3.2	64
33	A community-driven resource for genomic epidemiology and antimicrobial resistance prediction of <i>Neisseria gonorrhoeae</i> at Pathogenwatch. <i>Genome Medicine</i> , 2021, 13, 61.	8.2	63
34	Impact of Rapid Susceptibility Testing and Antibiotic Selection Strategy on the Emergence and Spread of Antibiotic Resistance in Gonorrhea. <i>Journal of Infectious Diseases</i> , 2017, 216, 1141-1149.	4.0	62
35	Cholera Modeling. <i>Epidemiology</i> , 2012, 23, 523-530.	2.7	61
36	Prediction of similarly acting cis-regulatory modules by subsequence profiling and comparative genomics in <i>Drosophila melanogaster</i> and <i>D.pseudoobscura</i> . <i>Bioinformatics</i> , 2004, 20, 2738-2750.	4.1	59

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37	Estimating SARS-CoV-2 seroprevalence and epidemiological parameters with uncertainty from serological surveys. <i>ELife</i> , 2021, 10, .	6.0	59
38	Trends in outpatient antibiotic use and prescribing practice among US older adults, 2011-15: observational study. <i>BMJ: British Medical Journal</i> , 2018, 362, k3155.	2.3	58
39	Genomic analyses of <i>Neisseria gonorrhoeae</i> reveal an association of the gonococcal genetic island with antimicrobial resistance. <i>Journal of Infection</i> , 2016, 73, 578-587.	3.3	54
40	Within-Host Whole-Genome Deep Sequencing and Diversity Analysis of Human Respiratory Syncytial Virus Infection Reveals Dynamics of Genomic Diversity in the Absence and Presence of Immune Pressure. <i>Journal of Virology</i> , 2014, 88, 7286-7293.	3.4	53
41	Poor Immunogenicity, Not Vaccine Strain Egg Adaptation, May Explain the Low H3N2 Influenza Vaccine Effectiveness in 2012-2013. <i>Clinical Infectious Diseases</i> , 2018, 67, 327-333.	5.8	53
42	Systematic analysis of protein identity between Zika virus and other arthropod-borne viruses. <i>Bulletin of the World Health Organization</i> , 2017, 95, 517-525I.	3.3	52
43	Weak Epistasis May Drive Adaptation in Recombining Bacteria. <i>Genetics</i> , 2018, 208, 1247-1260.	2.9	51
44	Adaptation to the cervical environment is associated with increased antibiotic susceptibility in <i>Neisseria gonorrhoeae</i> . <i>Nature Communications</i> , 2020, 11, 4126.	12.8	51
45	Azithromycin Susceptibility Among <i>Neisseria gonorrhoeae</i> Isolates and Seasonal Macrolide Use. <i>Journal of Infectious Diseases</i> , 2019, 219, 619-623.	4.0	41
46	Increased power from conditional bacterial genome-wide association identifies macrolide resistance mutations in <i>Neisseria gonorrhoeae</i> . <i>Nature Communications</i> , 2020, 11, 5374.	12.8	40
47	Improving Control of Antibiotic-Resistant Gonorrhea by Integrating Research Agendas Across Disciplines: Key Questions Arising From Mathematical Modeling. <i>Journal of Infectious Diseases</i> , 2016, 213, 883-890.	4.0	38
48	Trends in Antibiotic Susceptibility in <i>Staphylococcus aureus</i> in Boston, Massachusetts, from 2000 to 2014. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	3.9	37
49	Combining genomics and epidemiology to track mumps virus transmission in the United States. <i>PLoS Biology</i> , 2020, 18, e3000611.	5.6	37
50	SARS-CoV-2 Transmission Risk Among National Basketball Association Players, Staff, and Vendors Exposed to Individuals With Positive Test Results After COVID-19 Recovery During the 2020 Regular and Postseason. <i>JAMA Internal Medicine</i> , 2021, 181, 960-966.	5.1	32
51	Applications of genomics to slow the spread of multidrug-resistant <i>Neisseria gonorrhoeae</i> . <i>Annals of the New York Academy of Sciences</i> , 2019, 1435, 93-109.	3.8	31
52	RNA polymerase mutations cause cephalosporin resistance in clinical <i>Neisseria gonorrhoeae</i> isolates. <i>ELife</i> , 2020, 9, .	6.0	31
53	Fine-Scale Haplotype Structure Reveals Strong Signatures of Positive Selection in a Recombining Bacterial Pathogen. <i>Molecular Biology and Evolution</i> , 2020, 37, 417-428.	8.9	27
54	The role of "spillover" in antibiotic resistance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 29063-29068.	7.1	27

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55	Racial/Ethnic Disparities in Antimicrobial Drug Use, United States, 2014–2015. <i>Emerging Infectious Diseases</i> , 2018, 24, 2126-2128.	4.3	26
56	Identification of Hidden Population Structure in Time-Scaled Phylogenies. <i>Systematic Biology</i> , 2020, 69, 884-896.	5.6	26
57	Emergence and evolution of antimicrobial resistance genes and mutations in <i>Neisseria gonorrhoeae</i> . <i>Genome Medicine</i> , 2021, 13, 51.	8.2	25
58	Genomic Characterization of Urethritis-Associated <i>Neisseria meningitidis</i> Shows that a Wide Range of <i>N. meningitidis</i> Strains Can Cause Urethritis. <i>Journal of Clinical Microbiology</i> , 2017, 55, 3374-3383.	3.9	24
59	Use of whole-genome sequencing data to analyze 23S rRNA-mediated azithromycin resistance. <i>International Journal of Antimicrobial Agents</i> , 2017, 49, 252-254.	2.5	23
60	Building an international consortium for tracking coronavirus health status. <i>Nature Medicine</i> , 2020, 26, 1161-1165.	30.7	23
61	Impact of Species Diversity on the Design of RNA-Based Diagnostics for Antibiotic Resistance in <i>Neisseria gonorrhoeae</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	22
62	Modeling the impact of racial and ethnic disparities on COVID-19 epidemic dynamics. <i>ELife</i> , 2021, 10, .	6.0	22
63	Association Between COVID-19 Booster Vaccination and Omicron Infection in a Highly Vaccinated Cohort of Players and Staff in the National Basketball Association. <i>JAMA - Journal of the American Medical Association</i> , 2022, 328, 209.	7.4	21
64	<i>In Vitro</i> Selection of <i>Neisseria gonorrhoeae</i> Mutants with Elevated MIC Values and Increased Resistance to Cephalosporins. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 6986-6989.	3.2	20
65	The frontiers of addressing antibiotic resistance in <i>Neisseria gonorrhoeae</i> . <i>Translational Research</i> , 2020, 220, 122-137.	5.0	20
66	Case-based surveillance of antimicrobial resistance with full susceptibility profiles. <i>JAC-Antimicrobial Resistance</i> , 2019, 1, dlz070.	2.1	19
67	The Distribution and Spread of Susceptible and Resistant <i>Neisseria gonorrhoeae</i> Across Demographic Groups in a Major Metropolitan Center. <i>Clinical Infectious Diseases</i> , 2021, 73, e3146-e3155.	5.8	19
68	Implications of Test Characteristics and Population Seroprevalence on Immune Passport Strategies. <i>Clinical Infectious Diseases</i> , 2021, 72, e412-e414.	5.8	19
69	Outpatient Antibiotic Prescribing in Massachusetts, 2011–2015. <i>Open Forum Infectious Diseases</i> , 2019, 6, ofz169.	0.9	17
70	Genetic determinants of genus-level glycan diversity in a bacterial protein glycosylation system. <i>PLoS Genetics</i> , 2019, 15, e1008532.	3.5	16
71	Characterizing SARS-CoV-2 Viral Clearance Kinetics to Improve the Design of Antiviral Pharmacometric Studies. <i>Antimicrobial Agents and Chemotherapy</i> , 2022, 66, .	3.2	16
72	Surveillance to maintain the sensitivity of genotype-based antibiotic resistance diagnostics. <i>PLoS Biology</i> , 2019, 17, e3000547.	5.6	15

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73	Antimicrobial Resistance in <i>Neisseria gonorrhoeae</i> : Proceedings of the STAR Sexually Transmitted Infectionâ€™Clinical Trial Group Programmatic Meeting. <i>Sexually Transmitted Diseases</i> , 2019, 46, e18-e25.	1.7	15
74	Metagenomic Sequencing of an Echovirus 30 Genome From Cerebrospinal Fluid of a Patient With Aseptic Meningitis and Orchitis. <i>Open Forum Infectious Diseases</i> , 2017, 4, ofx138.	0.9	13
75	Testing for gonorrhoea should routinely include the pharynx. <i>Lancet Infectious Diseases</i> , The, 2018, 18, 716-717.	9.1	13
76	Deciphering the Impact of Bystander Selection for Antibiotic Resistance in <i>Neisseria gonorrhoeae</i> . <i>Journal of Infectious Diseases</i> , 2020, 221, 1033-1035.	4.0	13
77	Deciphering the Origins and Tracking the Evolution of Cholera Epidemics with Whole-Genome-Based Molecular Epidemiology. <i>MBio</i> , 2013, 4, e00670-13.	4.1	12
78	Efflux Pump Antibiotic Binding Site Mutations Are Associated with Azithromycin Nonsusceptibility in Clinical <i>Neisseria gonorrhoeae</i> Isolates. <i>MBio</i> , 2020, 11, .	4.1	12
79	K-Pax2: Bayesian identification of cluster-defining amino acid positions in large sequence datasets. <i>Microbial Genomics</i> , 2015, 1, e000025.	2.0	12
80	Analysis of multiple bacterial species and antibiotic classes reveals large variation in the association between seasonal antibiotic use and resistance. <i>PLoS Biology</i> , 2022, 20, e3001579.	5.6	12
81	Potential Biases Arising From Epidemic Dynamics in Observational Seroprotection Studies. <i>American Journal of Epidemiology</i> , 2021, 190, 328-335.	3.4	11
82	Loci for prediction of penicillin and tetracycline susceptibility in <i>Neisseria gonorrhoeae</i> : a genome-wide association study. <i>Lancet Microbe</i> , The, 2022, 3, e376-e381.	7.3	11
83	Deep sequencing of RSV from an adult challenge study and from naturally infected infants reveals heterogeneous diversification dynamics. <i>Virology</i> , 2017, 510, 289-296.	2.4	10
84	Potential impact of outpatient stewardship interventions on antibiotic exposures of common bacterial pathogens. <i>ELife</i> , 2020, 9, .	6.0	10
85	Multidrug-resistant <i>Neisseria gonorrhoeae</i> : implications for future treatment strategies. <i>Lancet Infectious Diseases</i> , The, 2018, 18, 599.	9.1	9
86	Severe Acute Respiratory Syndrome Coronavirus 2 Reinfection: A Case Series From a 12-Month Longitudinal Occupational Cohort. <i>Clinical Infectious Diseases</i> , 2022, 74, 1682-1685.	5.8	9
87	Biodiversity and hypervirulence of <i>Listeria monocytogenes</i> . <i>Nature Genetics</i> , 2016, 48, 229-230.	21.4	8
88	Using rapid point-of-care tests to inform antibiotic choice to mitigate drug resistance in gonorrhoea. <i>Eurosurveillance</i> , 2020, 25, .	7.0	8
89	Contrasting within- and between-host immune selection shapes <i>Neisseria Opa</i> repertoires. <i>Scientific Reports</i> , 2014, 4, 6554.	3.3	7
90	A Bayesian model of acquisition and clearance of bacterial colonization incorporating within-host variation. <i>PLoS Computational Biology</i> , 2019, 15, e1006534.	3.2	7

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91	Distinguishing the Roles of Antibiotic Stewardship and Reductions in Outpatient Visits in Generating a 5-Year Decline in Antibiotic Prescribing. <i>Clinical Infectious Diseases</i> , 2021, 72, 1568-1576.	5.8	7
92	Adaptive guidelines for the treatment of gonorrhoea to increase the effective life span of antibiotics among men who have sex with men in the United States: A mathematical modeling study. <i>PLoS Medicine</i> , 2020, 17, e1003077.	8.4	6
93	Childhood Respiratory Outpatient Visits Correlate With Socioeconomic Status and Drive Geographic Patterns in Antibiotic Prescribing. <i>Journal of Infectious Diseases</i> , 2021, 223, 2029-2037.	4.0	6
94	Targeted surveillance strategies for efficient detection of novel antibiotic resistance variants. <i>ELife</i> , 2020, 9, .	6.0	6
95	Cumulative Probability of Receiving an Antibiotic Prescription over Time. <i>New England Journal of Medicine</i> , 2019, 380, 1872-1873.	27.0	5
96	Disseminated Gonococcal Infection Complicated by Prosthetic Joint Infection: Case Report and Genomic and Phylogenetic Analysis. <i>Open Forum Infectious Diseases</i> , 2021, 8, ofaa632.	0.9	5
97	Interaction Patterns of Men Who Have Sex With Men on a Geosocial Networking Mobile App in Seven United States Metropolitan Areas: Observational Study. <i>Journal of Medical Internet Research</i> , 2019, 21, e13766.	4.3	5
98	ANTICIPATING RACIAL/ETHNIC MORTALITY DISPLACEMENT FROM COVID-19. <i>American Journal of Epidemiology</i> , 2022, 191, 1519-1520.	3.4	4
99	Modelling methicillin-resistant <i>Staphylococcus aureus</i> decolonization: interactions between body sites and the impact of site-specific clearance. <i>Journal of the Royal Society Interface</i> , 2022, 19, .	3.4	4
100	Identification of bile acid and fatty acid species as candidate rapidly bactericidal agents for topical treatment of gonorrhoea. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 2569-2577.	3.0	3
101	Trends in Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Seroprevalence in Massachusetts Estimated from Newborn Screening Specimens. <i>Clinical Infectious Diseases</i> , 2022, 75, e105-e113.	5.8	3
102	Epidemiology and genomics of a slow outbreak of methicillin-resistant <i>Staphylococcus aureus</i> (MRSA) in a neonatal intensive care unit: Successful chronic decolonization of MRSA-positive healthcare personnel. <i>Infection Control and Hospital Epidemiology</i> , 2023, 44, 589-596.	1.8	3
103	Reply to Guy et al.: Support for a bottleneck in the 2011 <i>Escherichia coli</i> O104:H4 outbreak in Germany. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E3629-E3630.	7.1	2
104	Sculpting the Bacterial <i>O</i> -Glycoproteome: Functional Analyses of Orthologous Oligosaccharyltransferases with Diverse Targeting Specificities. <i>MBio</i> , 2022, 13, e0379721.	4.1	2
105	A Patient with Fevers and Fatigue. <i>New England Journal of Medicine</i> , 2013, 368, e9.	27.0	1
106	Bitter Pills. <i>New England Journal of Medicine</i> , 2010, 363, e26.	27.0	1
107	Bridging of <i>Neisseria Gonorrhoeae</i> Across Diverse Sexual Networks in the HIV Pre-Exposure Prophylaxis (PrEP) Era: A Clinical and Molecular Epidemiological Study. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
108	Response to comment on 'The distribution of antibiotic use and its association with antibiotic resistance'. <i>ELife</i> , 2019, 8, .	6.0	1

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109	Evaluating spatially adaptive guidelines for the treatment of gonorrhea to reduce the incidence of gonococcal infection and increase the effective lifespan of antibiotics. PLoS Computational Biology, 2022, 18, e1009842.	3.2	1
110	Bitter Pills. New England Journal of Medicine, 2010, 363, 1847-1851.	27.0	0
111	Vaccine waning and mumps re-emergence in the USA. Open Forum Infectious Diseases, 2017, 4, S25-S25.	0.9	0
112	Response to Skowronski and De Serres. Clinical Infectious Diseases, 2018, 67, 1476-1476.	5.8	0
113	Reduction in Antibiotic Prescribing Attainable With a Gonococcal Vaccine. Clinical Infectious Diseases, 2021, 73, e1368-e1371.	5.8	0
114	Post-discharge decolonization of patients harboring methicillin-resistant <i>Staphylococcus aureus</i> (MRSA) USA300 strains: secondary analysis of the CLEAR Trial. Infection Control and Hospital Epidemiology, 2021, , 1-4.	1.8	0
115	Combining genomics and epidemiology to track mumps virus transmission in the United States. , 2020, 18, e3000611.		0
116	Combining genomics and epidemiology to track mumps virus transmission in the United States. , 2020, 18, e3000611.		0
117	Combining genomics and epidemiology to track mumps virus transmission in the United States. , 2020, 18, e3000611.		0
118	Combining genomics and epidemiology to track mumps virus transmission in the United States. , 2020, 18, e3000611.		0
119	Combining genomics and epidemiology to track mumps virus transmission in the United States. , 2020, 18, e3000611.		0
120	Combining genomics and epidemiology to track mumps virus transmission in the United States. , 2020, 18, e3000611.		0
121	Title is missing!. , 2020, 17, e1003077.		0
122	Title is missing!. , 2020, 17, e1003077.		0
123	Title is missing!. , 2020, 17, e1003077.		0
124	Title is missing!. , 2020, 17, e1003077.		0